

**AMENDMENTS TO THE CLAIMS**

1.– 13. (Cancelled)

14. (Currently Amended) A computer-implemented method of generating a local-global alignment score which indicates a global and a local similarity between a first protein structure and a second protein structure, the method executed by one or more computer systems and comprising:

receiving, at the one or more computer systems, a protein structure correspondence wherein a plurality of positions in the protein structure correspondence indicates a corresponding pair of residues in the first protein structure and the second protein structure;

the one or more computer systems determining a plurality of root mean square deviations corresponding to a plurality of sets of pairs of residues, wherein each set of pairs of residues comprises a plurality of pairs of residues that are contiguous in the protein structure correspondences and the plurality of root mean square deviations are determined using a plurality of specified threshold values;

the one or more computer systems selecting a longest contiguous segment corresponding to a set of pairs of residues of the plurality of pairs of residues based on the plurality of root mean square deviations

the one or more computer systems identifying a plurality of distance scores, wherein each distance score corresponds to a number of pairs of residues in the correspondence that are within a pre-defined distance of a plurality of pre-defined distances  
the one or more computer systems selecting a global distance test value based on the plurality of distance scores;  
the one or more computer systems generating the local-global alignment score based on the longest contiguous segment and the global distance test value ; and  
the one or more computer systems providing a result based on the local-global alignment score.

15. (Cancelled)

16. (Cancelled)

17. (Cancelled)

18. (Cancelled)

19. (Currently Amended) The method of claim 14, wherein the one or more computer systems comprise a server and further comprising:

receiving, at a server, a first set of co-ordinates associated with the first protein structure from a client;

receiving, at the server, a second set of co-ordinates associated the second protein structure; and

the server generating, ~~at the server,~~ the protein structure correspondence  
based on the first set of co-ordinates and the second set of co-  
ordinates.

20. (Currently Amended) The method of claim 14, further comprising:  
receiving, at the one or more computer systems, a first set of co-ordinates  
associated with the first protein structure;  
receiving, at the one or more computer systems, a second set of co-ordinates  
associated the second protein structure; and  
the one or more computer systems generating the protein structure  
correspondence based on the first set of co-ordinates and the second  
set of co-ordinates.

21. (Currently Amended) The method of claim 20, wherein providing a result  
based on the local-global alignment score further comprises:  
the one or more computer systems generating a second protein structure  
correspondence based on the local-global alignment score; and  
the one or more computer systems providing the second protein structure  
correspondence.

22. (Currently Amended) The method of claim 20, wherein providing the second  
protein structure correspondence comprises:

the one or more computer systems modifying the set of co-ordinates

specifying the first protein structure based on at last one of the global

distance test value and the longest continuous segment to generate a

second set of co-ordinates specifying the first protein structure; and

the one or more computer systems providing the second ~~modified~~ set of co-ordinates.

23. (Currently Amended) The method of claim 21, wherein providing the second protein structure correspondence comprises:

the one or more computer systems displaying a graphical representation of at

least one of the first protein structure or the second protein structure,

wherein at least some of the residues in the graphical representation

are colored according to distance between the at last some of the

residues and the corresponding residues in the second protein

structure.

24. (Previously Presented) The method of claim 23, wherein the graphical representation is a bar plot.

25. (Previously Presented) The method of claim 23, wherein the graphical representation is a three-dimensional protein structure.